

1 ATTCTCCCATTCTCCCTCCCTCTCCCTTCTCCCTCTCCACTGGCTCCTCGTTTCTCTCC 60
61 ATCTGCCTGACTCCTTGGGACCCGGTCCCCAGCTCGAGGATGGCGTCCTCTCTGCTTGAG 120
M A S S L L E 7
121 GAAGAAGCTCACTATGGCTCCAGTCCCCTGGCCATGCTGACTGCAGCCTGCAGCAAATTT 180
8 E E A H Y G S S P L A M L T A A C S K F 27
181 GGCGGCTCTAGCCCTCTGCGGGACTCAACAACCCTGGGGAAAGGAGGCACAAAGAAGCCA 240
28 G G S S P L R D S T T L G K G G T K K P 47
241 TACGCTGACCTTTTCAAGCCCCAAAACCATGGGGGACGCCTACCCAGCTCCCTTCTCAAGC 300
48 Y A D L S A P K T M G D A Y P A P F S S 67
301 ACCAATGGACTCCTCTCTCCTGCAGGCAGTCTCCGGCCCCAGCCTCTGGCTATGCAAT 360
68 T N G L L S P A G S P P A P A S G Y A N 87
361 GACTACCCACCCTTCCCTCACTCATTTCCTGGGCCCACCGGTGCCCAAGACCCTGGGCTC 420
88 D Y P P F P H S F P G P T F A Q D P G L 107
421 CTAGTGCCTAAGGGGGACAGCTCGTCTGACTGCCTGCTAGTGTCTACACTTCCCTGGAT 480
108 L V P K G K S S S D C L P S V Y T S L D 127
481 ATGACTCATCCCTATGGCTCGTGGTACAAGGCAGGCATCCACGCAGGCATCTCACCAGGT 540
128 M T H P Y G S W Y K A G I K A G I S P G 147
541 CCAGGCAACACACCTACTCCTTGGTGGGACATGCACCCTGGGGGCAACTGGCTAGGTGGT 600
148 P G N T P T P W W D M H P G G N W L G G 167
601 GGTCAGGGCCAGGGTGATGGGCTGCAAGGGACACTGTCCACAGGCCCTGCCAGCCTCCA 660
168 G Q G Q G D G L Q G T L S T G P A Q P P 187
661 CTGAACCCCCAGCTGCCTACTTACCCATCTGACTTTGCTCCCCTTAACCCAGCTCCCTAC 720
188 L N P Q L P T Y P S D F A P L N P A P Y 207
721 CCAGCGCCCCACCTCTTGCAACCAGGGCCCCAGCATGTCCTACCCCAAGATGTCTATAAG 780
208 P A P H L L Q P G P Q H V L P Q D V Y K 227
781 CCAAGGCGGTTGGCAATAGTGGGCAACTGGAGGGGAGTGGTGCAGCCAAACCCCTCGG 840
228 P K A V G N S G Q L E G S G A A K P P R 247
841 GGTGCTGGCACAGGGGGCAGCGGTGGATATGCGGGCAGTGGGGCAGGGCGTTCTACCTGC 900
248 G A G T G G S G G Y A G S G A G R S T C 267
901 GACTGCCCCAACTGTCAGGAGCTAGAGCGGCTCGGGGCAGCAGCGGCTGGGCTGAGGAAG 960
268 D C P N C Q E L E R L G A A A A G L R K 287
961 AAGCCCATTACAGCTGCCACATCCCTGGGTGCGGCAAGGTGTACGGCAAGGCTTCGCAT 1020
288 K P I H S C H I P G C G K V Y G K A S H 307
1021 CTGAAAGCCCCTTGCCTGGCAGCTGGCGAGAGGCCTTTTCGTCTGCAACTGGCTTTTC 1080
308 L K A H L R W H T G E R P F V C N W L F 327
1081 TCGGCAAGAGGTTCACTCGCTCTGACGAGCTGGAGCGCCACGTGCGCACTCACACCCGG 1140
328 C G K R F T R S D E L E R H V R T H T R 347
1141 GAGAAGAAGTTCACTTGCCTGCTCTGTTCCAAGCGCTTTACCAGAAGCGACCACTTGAGC 1200
348 E K K F T C L L C S K R F T R S D H L S 367
1201 AAACATCAGCGCACCCACGGGGAGCCAGGCCCGGGACCGCCCCCAAGTGGCCCTAAGGAG 1260
368 K H Q R T H G E P G P G P P P S G P K E 387

FIG. 1A-1

1261 CTGGGGGAGGGTCGCAGCGTCGGGGAAGAAGAAGCCAATCAGCCGCCCCGATCTTCCACT 1320
 388 L G E G R S V G E E E A N Q P P R S S T 407
 1321 TCGCCTGCACCCCCAGAAAAAGCCCACGGAGGCAGCCAGAGCAGAGCAACCTGCTAGAG 1380
 408 S P A P P E K A H G G S P E Q S N L L E 427
 1381 ATCTGAGCCGGGTAGAGGAAGGTCTCCAGCTCCAGGGTCCTCTTGCCAGGCTCTCTTGGC 1440
 428 I *
 1441 GTGCTGGACCCATTGGTTGCCCCTCGCTCTCTCCTATTGCATGCTATACTCTGGGGGCTC 1500
 1501 TCTCTGTTCCCCTAGGCTATCTCCTTGCATGTCTCCTCAGTTCTTCTCTCTTTGTCAAGA 1560
 1561 GTCTTAGCCAAACTCCTCTCAGGCCTTTGCCAGTGCCTAGTTCCTATGCTCCGACCTCCT 1620
 1621 CAACTTTTTTCTTCTCTGCCCCTGTTCTTCACAGCTTCCATCTGGCCTCACATCATTTTTCT 1680
 1681 CATTAACTCGTTGCCATCTAATCTTTCTGCTTCCCAATCCTATTTGCCGTTTTCCCGAAG 1740
 1741 CTTCCAGGCTGTGCGCTCGATTCCCCCCCACCTTTTCGTCTTCCTGAGCTTTGTGTTTTCT 1800
 1801 TTTTTTAAACAAACACGATGATGATGATGATGATGATAATTTATTGCCCCCTGGTGT 1860
 1861 TCTTCATTAGGAACCAGAGTTAAGGAGATTGGTGTTAGTAACCTGGCCGGGAGCAGAGTG 1920
 1921 CCAAGAAGGGGGAAGTCCAATGGGGATCTGATCCCAAAGATGGGGTGACCCCAGGGTCAG 1980
 1981 GGAGGCTGCCCCAGCCTTGAGTACTTAACCCCTATGCGCCAGGAGTAAAGAATAGTAAT 2040
 2041 AGTAATAATAATAATAATTCTATTTATCTAAGTTATGATGACGGGTCAGGTACAGTGAGC 2100
 2101 TGGAGAGGGGAAAGGGATTCTCCCCGCCCCCAAGGAAATTCTAGTCAAATGCATCTCTGTA 2160
 2161 TAGACAAATGATAGTGAGACCTTGCTCGTAGATTTCTATCCTCGAGGTCTCCGAGAGTT 2220
 2221 TCTTTTTTCAGTTGAGTTTTGGGTTGTTTCGGCCTCTTTTAGAGTTTCTGTGGGTGTCTCTC 2280
 2281 TGTTAGGCAGTCACTAAGATCCCCAGCCCCAGCCAGAAAGCTGTGAAACTTCAAGTCCTA 2340
 2341 TGGCGGGGAGGACTGGAATGTACCCAGTCCTCTCGACCCGACTGCAGATCAGGTTCCCTC 2400
 2401 CCCTGATCCTCTTCTCATACCCTGTGACCTCACCAGGTTATCCCCTTGTGTCATGGTTA 2460
 2461 CAGAGAGCTTGCAGCTGCCATCTTAAACGTGCTCTTTGGGGGAGAGCCACCTAACAGGA 2520
 2521 GGATTTTGGTTTGGAGGTGCCCCTCCTGAAAAAGTAGGTGGGCAAAGGCTTTCTCTGGGA 2580
 2581 TCAAATTCAAATAAATCAAGTATTTATTGAATGCTTAATATGTGCAAGGCCTGGTGCCTA 2640
 2641 GAAGCCACGAGAAAGAATTTATAACAGGACAGAAGTCCCTAAACTAAACATCCACAGGCC 2700
 2701 CCCAATCTAGGAGGTTTCACTCCATTCCAGTGACTTTTAAAGCCGCTTTGTGCCTTTGAA 2760
 2761 ATGCCTTTCTGAGATTTTTTGGATCTTCCTGTTCTGTCCCCTGCTCCTTCTAGGCCTCAA 2820
 2821 GATAAAGGGTAAAGCCATGGAGTCTGGGAAGAGCATAACGTCGTTGACGGGATCGTCCCT 2880
 2881 TTGTGGAATCTTTCTTTTTTTTTTAAATTAATAAATAAAAGTTCGATTTCAAAAAAAAAA 2900
 2901 AAAAAAAAAAAAAAAAAAAAAA 2960

FIG. 1A-2

% IDENTITY

[illegible]

FIG. 1B

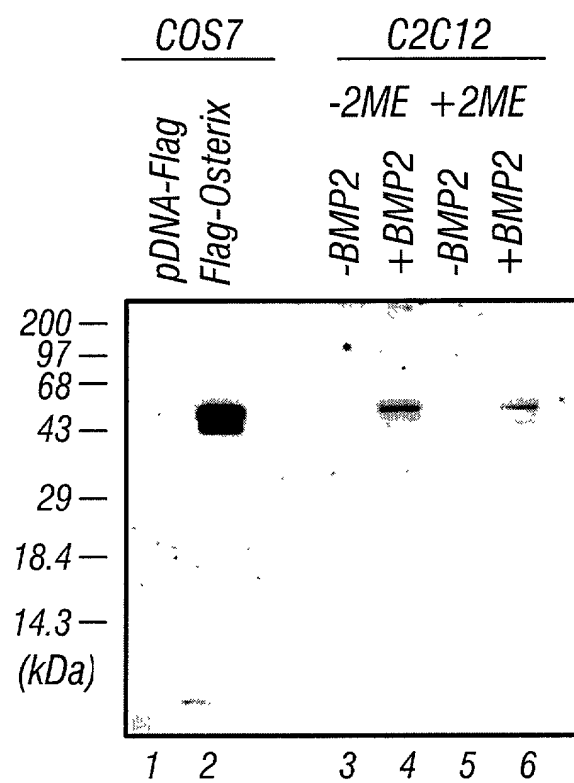


FIG. 2

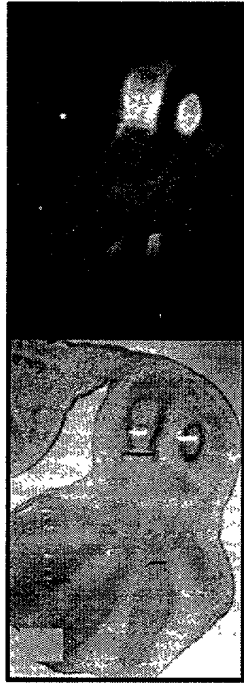


FIG. 3A

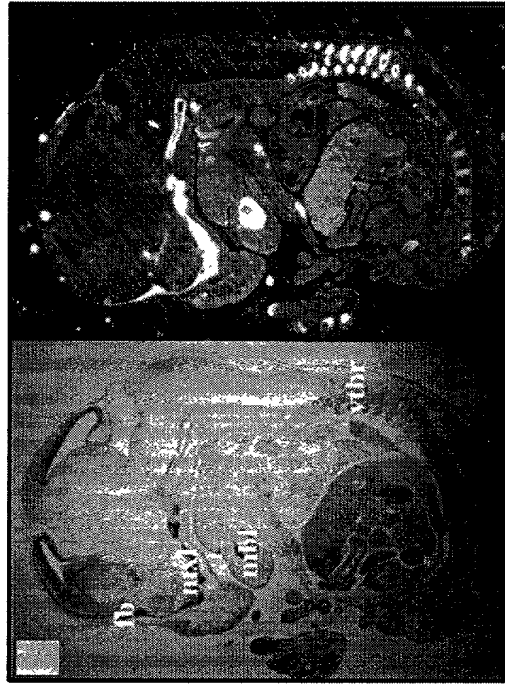


FIG. 3B

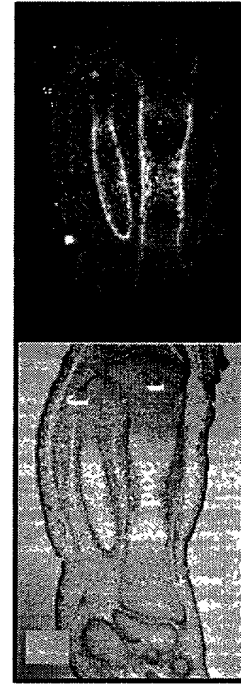


FIG. 3C

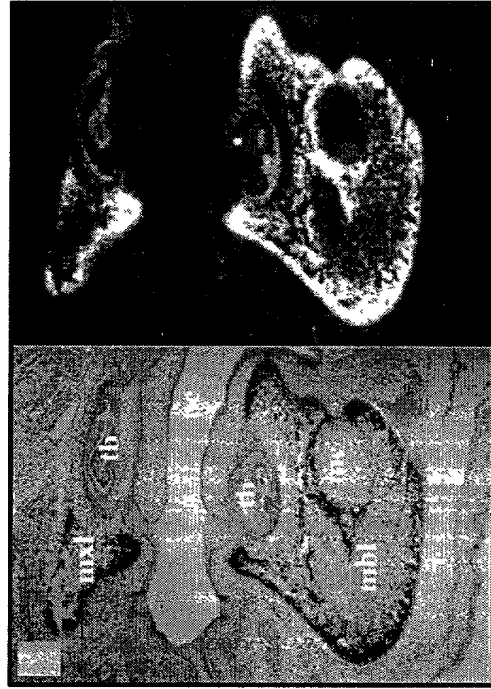


FIG. 3D

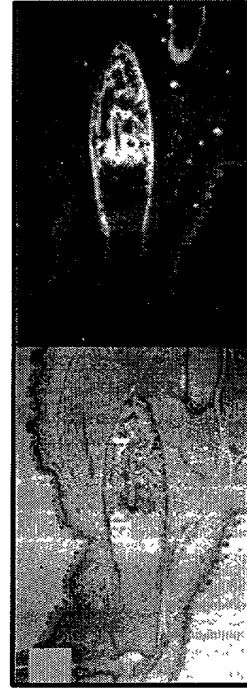


FIG. 3E

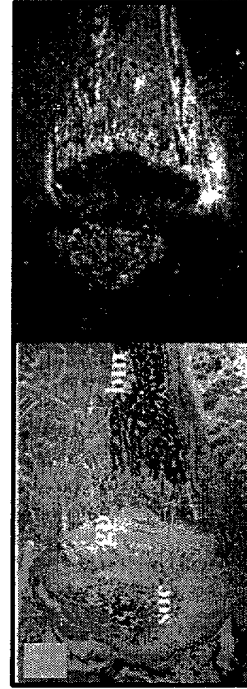


FIG. 3F

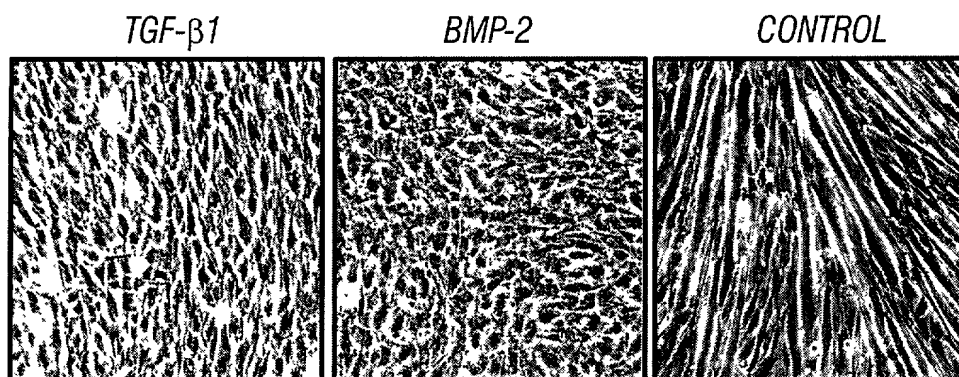


FIG. 4A

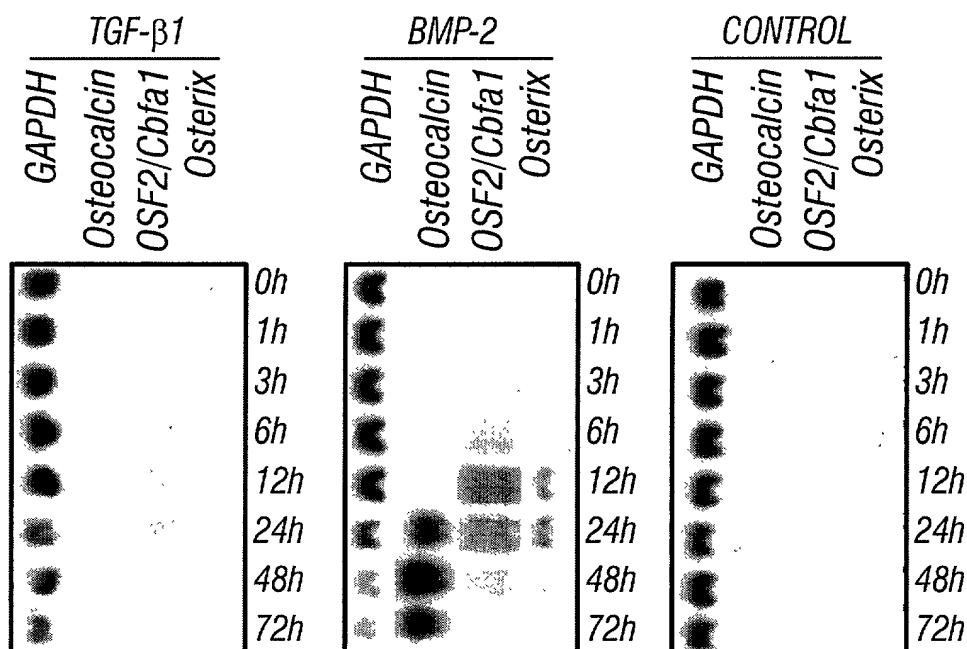


FIG. 4B

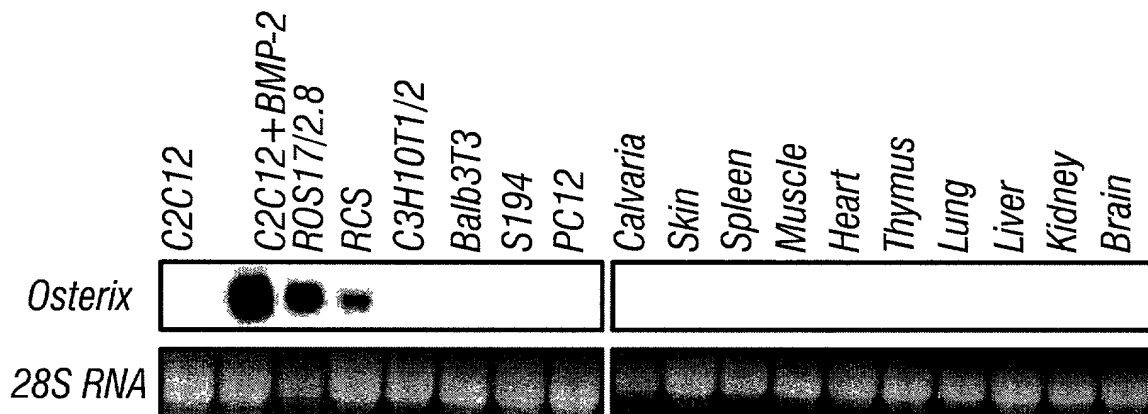


FIG. 4C

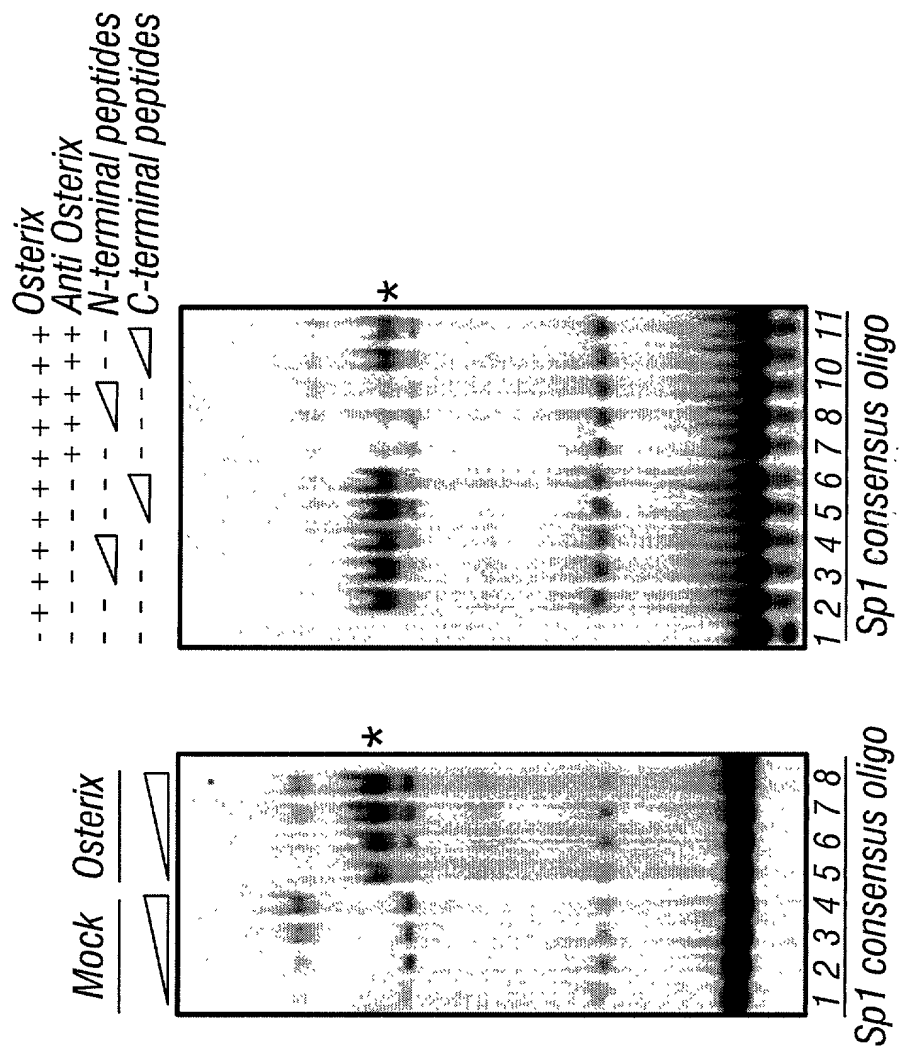


FIG. 5A

FIG. 5B

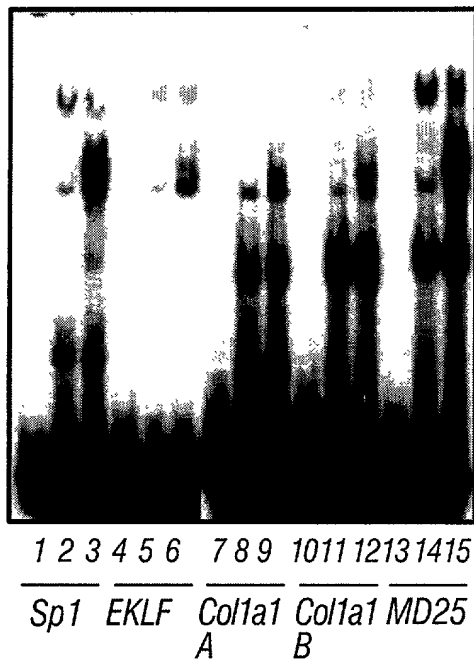


FIG. 6A

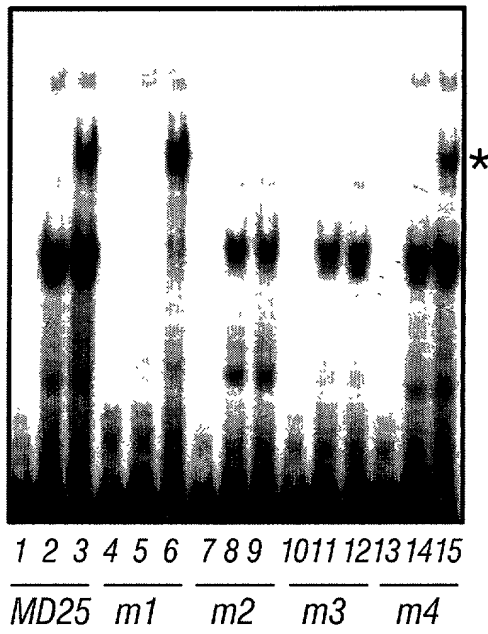


FIG. 6B

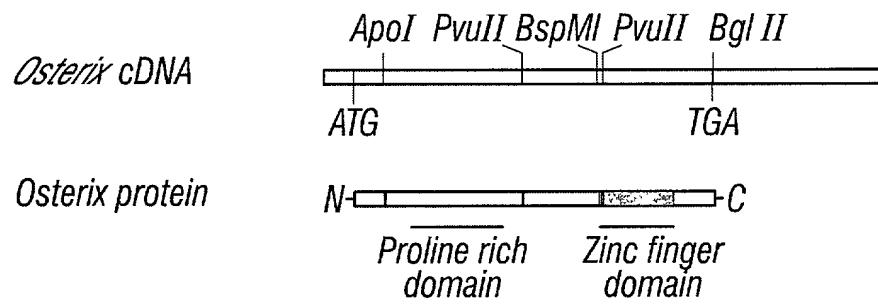


FIG. 7A

<u>Constructs</u>	<u>Transcriptional activity</u>
gal4(1-147)	1.0
pSGC22(27-428)	3.0
pSGC22(27-270)	127.3
pSGC22(27-192)	68.4
pSGC22(192-291)	0.6
pSGC22(293-428)	0.5

FIG. 7B

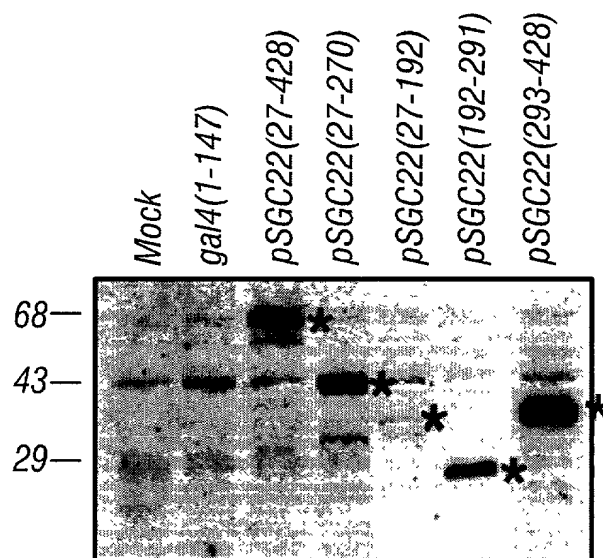


FIG. 7C

BSS Chromosome 15

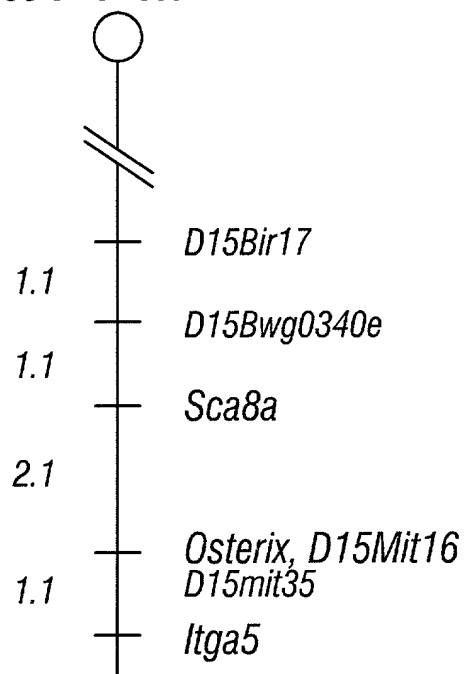


FIG. 8A

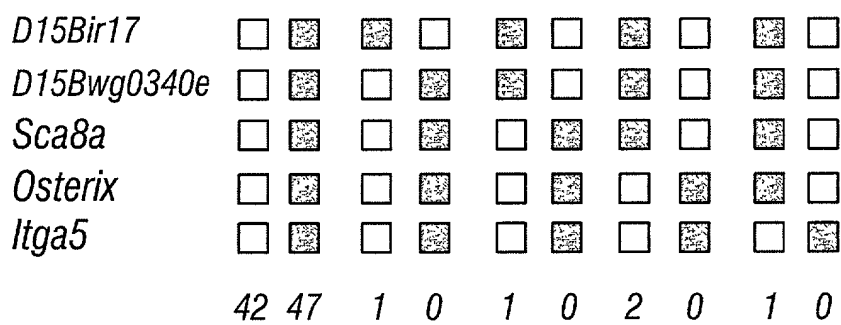


FIG. 8B

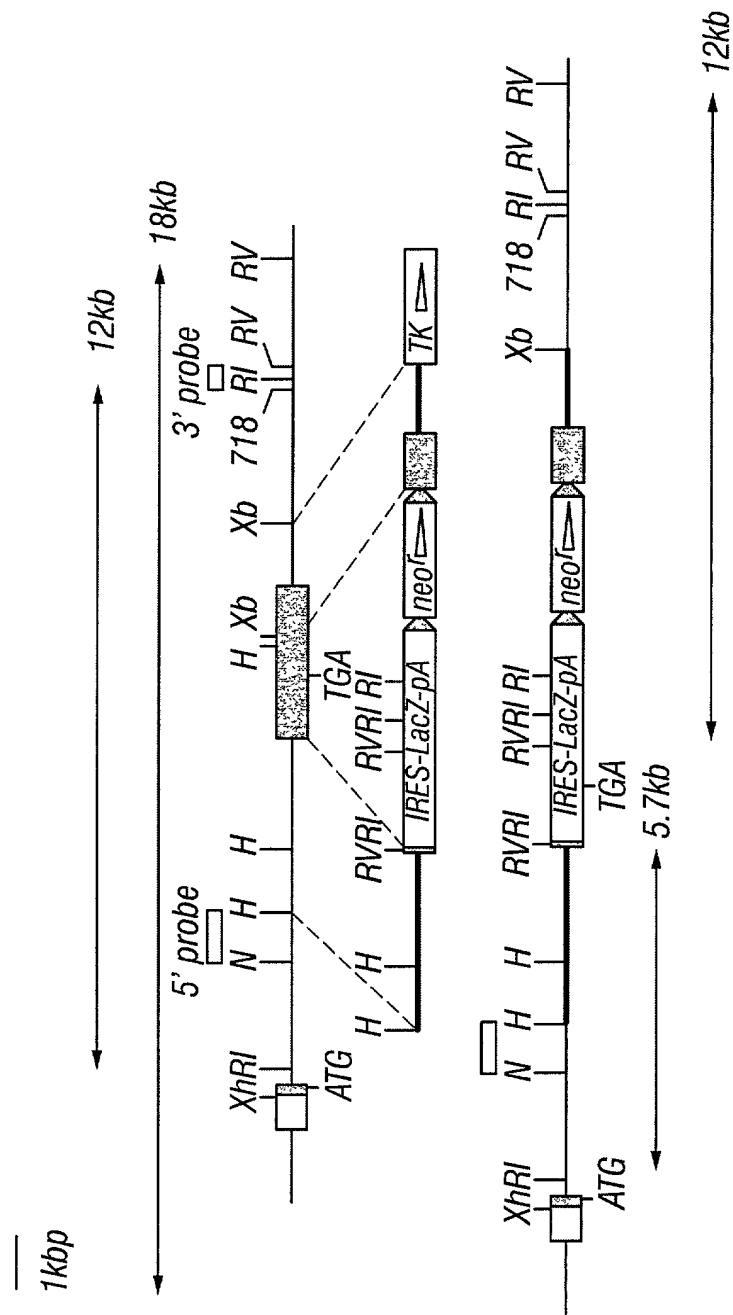


FIG. 8

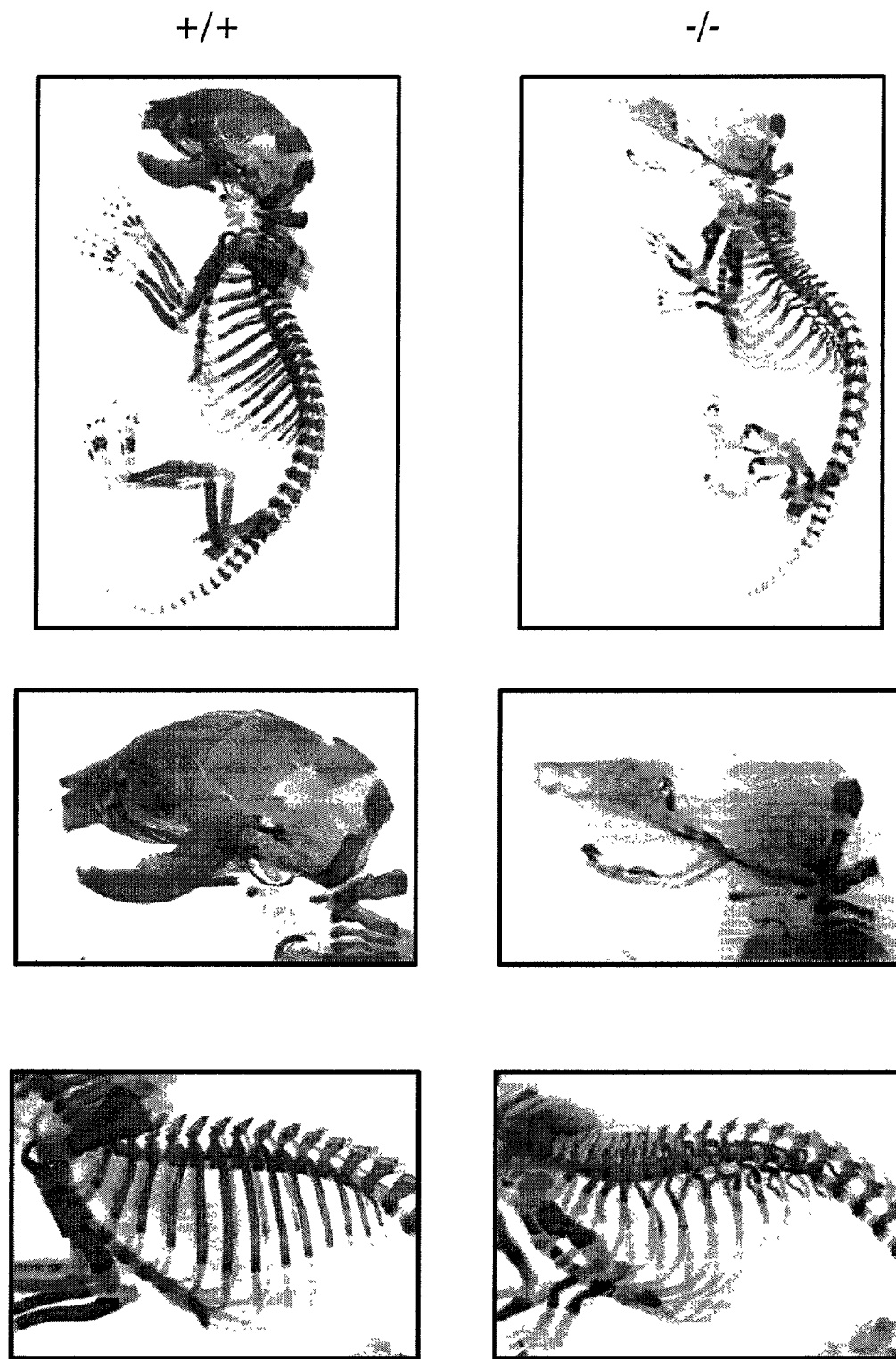


FIG. 9

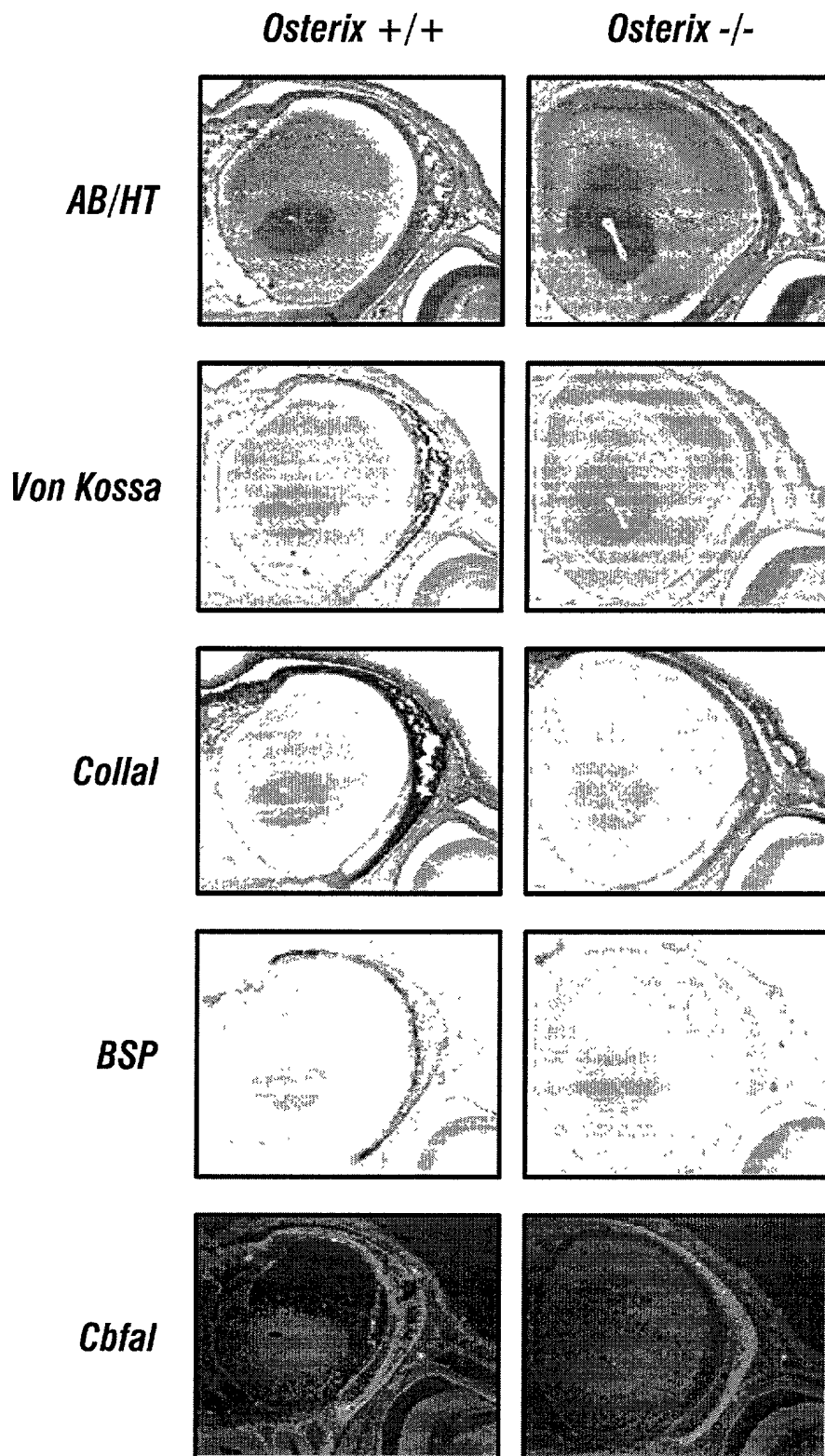


FIG. 10A

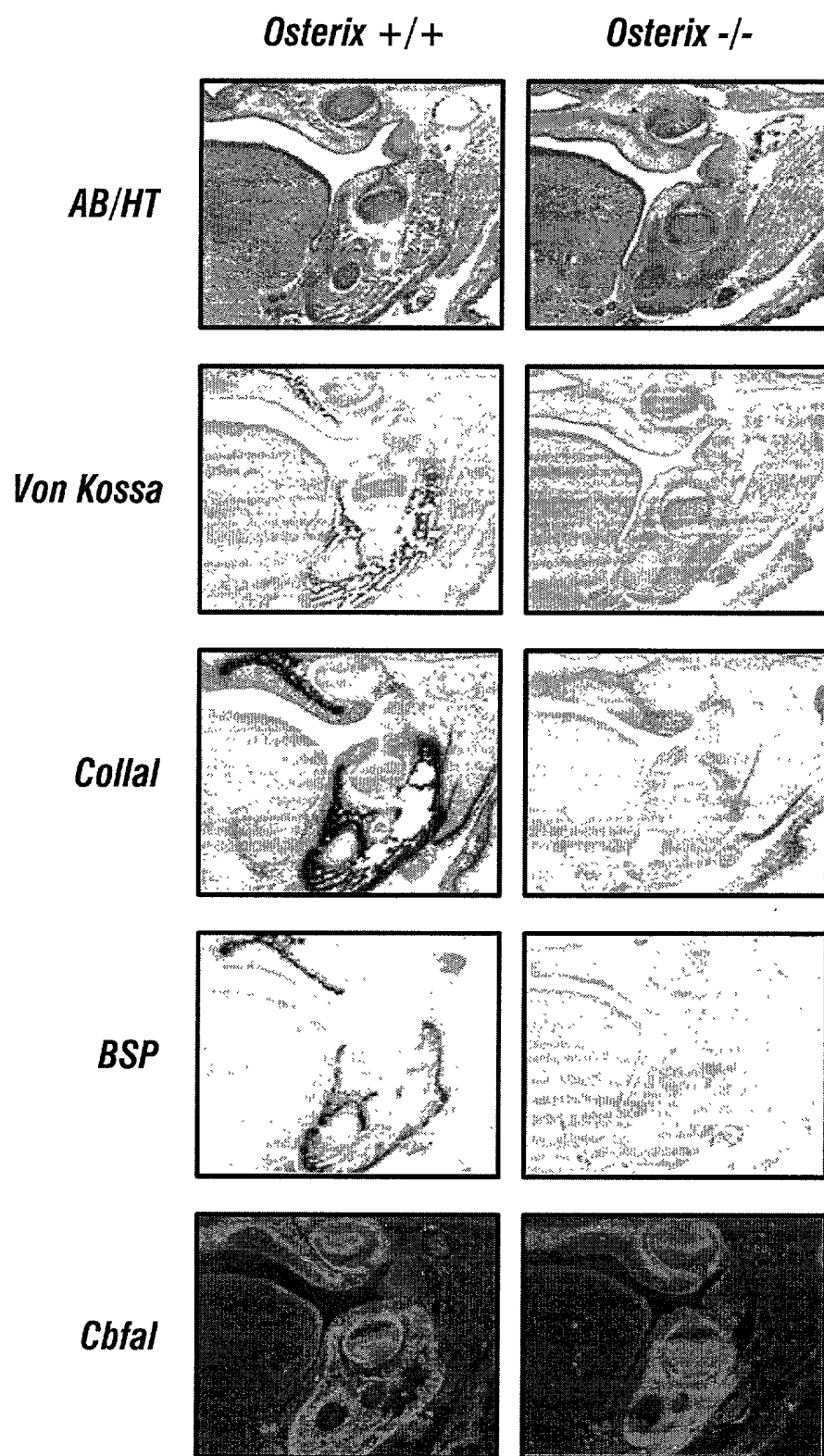


FIG. 10B

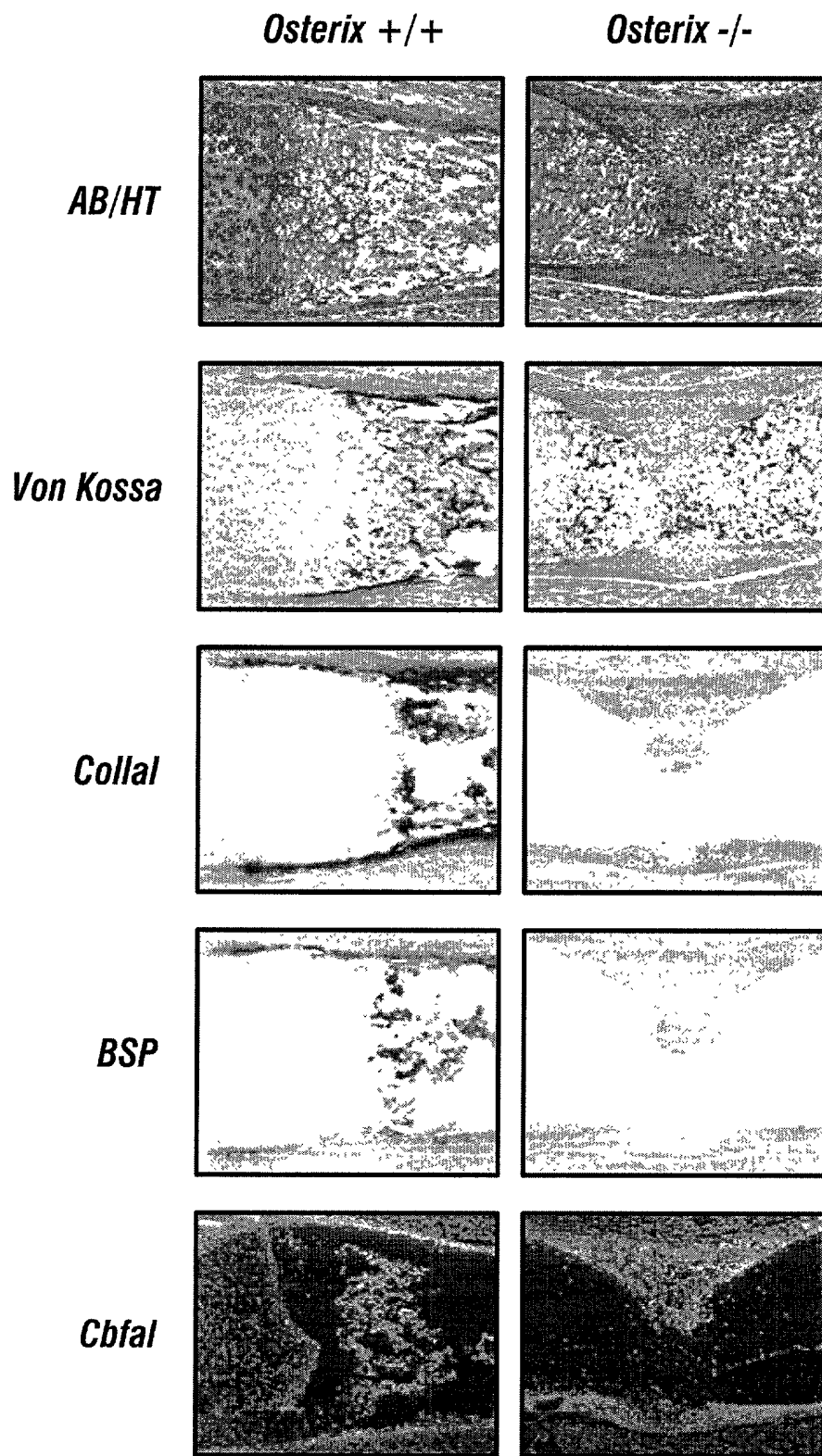


FIG. 10C

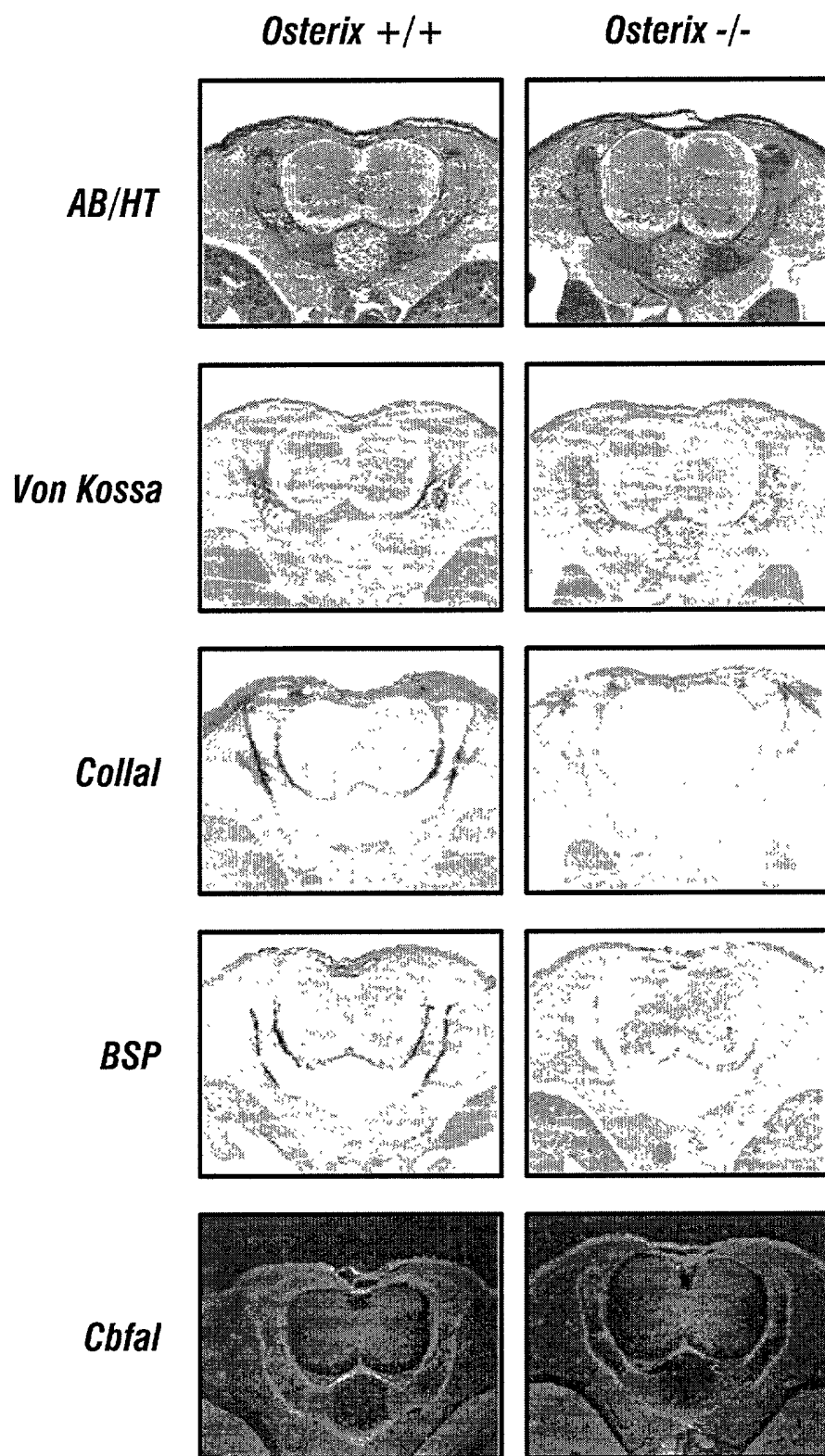


FIG. 10D